SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:

        (A) NAME: Eurogene Limited

        (B) STREET: Marquis House, 67/68 Jermyn Street

        (C) CITY: London

        (E) COUNTRY: United Kingdom

        (F) POSTAL CODE (ZIP): SW1Y 6NY

    (ii) TITLE OF INVENTION: BIOTIN-BINDING RECEPTOR MOLECULES

    (iii) NUMBER OF SEQUENCES: 2

    (iv) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: Floppy disk

        (B) COMPUTER: IBM PC compatible

        (C) OPERATING SYSTEM: PC-DOS/MS-DOS

        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 5177 base pairs

        (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:

        (A) NAME/KEY: CDS

        (B) LOCATION:1071..2270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAGT AACGCCACTT TGCAAGGCAT        60

GGAAAAATAC ATAACTGAGA ATAGAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC         120

TGAATACCAA ACAGGATATC TGTGGTAAGC GGTTCCTGCC CCGGCTCAGG GCCAAGAACA        180

GATGAGACAG CTGAGTGATG GGCCAAACAG GATATCTGTG GTAAGCAGTT CCTGCCCCGG        240

CTCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC CCTCAGCAGT TTCTAGTGAA        300

TCATCAGATG TTTCCAGGGT GCCCCAAGGA CCTGAAAATG ACCCTGTACC TTATTTGAAC        360

TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA        420

AGAGCCCACA ACCCCTCACT CGGCGCGCCA GTCTTCCGAT AGACTGCGTC GCCCGGGTAC        480

CCGTATTCCC AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCTTG        540

GGAGGGTCTC CTCTGAGTGA TTGACTACCC ACGACGGGGG TCTTTCATTT GGGGGCTCGT        600

CCGGGATTTG GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG TAAGCTGGCC        660

AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG TTTGATGTTA TGCGCCTGCG        720

TCTGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC CGTGGTGGAA CTGACGAGTT        780

CTGAACACCC GGCCGCAACC CTGGGAGACG TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG        840

CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT        900

AGGAGACGAG AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA        960

CCGAAGCCGC GCGTCTTGTC TGCTGCAGCC AAGCTTGGGC TGCAGGTCGA CTCTAGAGGA       1020
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TCAATTCGGC ACGAGTAAAT CGGTGCTGCC GTCTTTAGGA CATATGAAGT ATG GCA   1076
                                                              Met Ala
                                                               1

CAG TGG GAT GAC TTT CCT GAT CAG CAA GAG GAC ACT GAC AGC TGT ACA   1124
Gln Trp Asp Asp Phe Pro Asp Gln Gln Glu Asp Thr Asp Ser Cys Thr
         5   10   15

GAG TCT GTG AAG TTC GAT GCT CGC TCA GTG ACA GCT TTG CTT CCT CCC   1172
Glu Ser Val Lys Phe Asp Ala Arg Ser Val Thr Ala Leu Leu Pro Pro
         20   25   30

CAT CCT AAA AAT GGC CCA ACT CTT CAA GAG AGG ATG AAG TCT TAT AAA   1220
His Pro Lys Asn Gly Pro Thr Leu Gln Glu Arg Met Lys Ser Tyr Lys
 35   40   45   50

ACT GCA CTG ATC ACC CTT TAT CTC ATT GTG TTT GTA GTT CTC GTG CCC   1268
Thr Ala Leu Ile Thr Leu Tyr Leu Ile Val Phe Val Val Leu Val Pro
                 55   60   65

ATC ATT GGC ATA GTG GCA GCT CAG CTC CTG AAA TGG GAA ACG AAG AAT   1316
Ile Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr Lys Asn
                 70   75   80

TGC ACG GTT GGC TCA GTT AAT GCA GAT ATA TCT CCA AGT CCG GAA GGC   1364
Cys Thr Val Gly Ser Val Asn Ala Asp Ile Ser Pro Ser Pro Glu Gly
             85   90   95

AAA GGA AAT GGC AGT GAA GAT GAA ATG AGA TTT CGA GAA GCT GTG ATG   1412
Lys Gly Asn Gly Ser Glu Asp Glu Met Arg Phe Arg Glu Ala Val Met
 100   105   110

GAA CGC ATG AGC AAC ATG GAA AGC AGA ATC CAG TAT CTT TCA GAT AAT   1460
Glu Arg Met Ser Asn Met Glu Ser Arg Ile Gln Tyr Leu Ser Asp Asn
115   120   125   130

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GAA GCC AAT CTC CTA GAT GCT AAG AAT TTC CAA AAT TTC AGC ATA ACA          1508
Glu Ala Asn Leu Leu Asp Ala Lys Asn Phe Gln Asn Phe Ser Ile Thr
                135                 140                 145


ACT GAT CAA AGA TTT AAT GAT GTT CTT TTC CAG CTA AAT TCC TTA CTT          1556
Thr Asp Gln Arg Phe Asn Asp Val Leu Phe Gln Leu Asn Ser Leu Leu
                150                 155                 160


TCC TCC ATC CAG GAA CAT GAG AAT ATC ATA GGG GAT ATC TCC AAG TCA          1604
Ser Ser Ile Gln Glu His Glu Asn Ile Ile Gly Asp Ile Ser Lys Ser
        165                 170                 175


TTA GTA GGT CTG AAC ACC ACA GTA CTT GAT TTG CAG TTC AGT ATT GAA          1652
Leu Val Gly Leu Asn Thr Thr Val Leu Asp Leu Gln Phe Ser Ile Glu
        180                 185                 190


ACA CTG AAT GGC AGA GTC CAA GAG AAT GCA TTT AAA CAA CAA GAG GAG          1700
Thr Leu Asn Gly Arg Val Gln Glu Asn Ala Phe Lys Gln Gln Glu Glu
195                 200                 205                 210


ATG CGT AAA TTA GAG GAG CGT ATA TAC AAT GCA TCA GCA GAA ATT AAG          1748
Met Arg Lys Leu Glu Glu Arg Ile Tyr Asn Ala Ser Ala Glu Ile Lys
                215                 220                 225


TCT CTA GAT GAA AAA CAA GTA TAT TTG GAA CAG GAA ATA AAA GGG GAA          1796
Ser Leu Asp Glu Lys Gln Val Tyr Leu Glu Gln Glu Ile Lys Gly Glu
                230                 235                 240


ATG AAA CTG TTG AAT AAT ATC ACT AAT GAT CTG AGG CTG AAG GAT TGG          1844
Met Lys Leu Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu Lys Asp Trp
        245                 250                 255


GAA CAT TCT CAG ACA TTG AAA AAT ATC ACT TTA CTC CAA GGT GCC AGA          1892
Glu His Ser Gln Thr Leu Lys Asn Ile Thr Leu Leu Gln Gly Ala Arg
        260                 265                 270
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AAG TGC TCG CTG ACT GGG AAA TGG ACC AAC GAT CTG GGC TCC AAC ATG      1940
Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met
275             280             285             290


ACC ATC GGG GCT GTG AAC AGC AGA GGT GAA TTC ACA GGC ACC TAC ATC      1988
Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile
            295             300             305


ACA GCC GTA ACA GCC ACA TCA AAT GAG ATC AAA GAG TCA CCA CTG CAT      2036
Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro Leu His
            310             315             320


GGG ACA CAA AAC ACC ATC AAC AAG AGG ACC CAG CCC ACC TTT GGC TTC      2084
Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe
            325             330             335


ACC GTC AAT TGG AAG TTT TCA GAG TCC ACC ACT GTC TTC ACG GGC CAG      2132
Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln
            340             345             350


TGC TTC ATA GAC AGG AAT GGG AAG GAG GTC CTG AAG ACC ATG TGG CTG      2180
Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu
355             360             365             370


CTG CGG TCA AGT GTT AAT GAC ATT GGT GAT GAC TGG AAA GCT ACC AGG      2228
Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg
            375             380             385


GTC GGC ATC AAC ATC TTC ACT CGC CTG CGC ACA CAG AAG GAG             2270
Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu
            390             395             400


TGAGTGAGTG ACCAAGGTCC TCCTGGACTC CAGGTGAAAA AGGAGATAGA GGCCCTCCTG     2330


GACAAAATGG TATACCAGGC TTTCCAGGTC TAATAGGTAC TCCAGGTCTT AAAGGTGATC     2390


GGGGGGATCT CTGGTTTACC TGGAGTTCGA GGATTCCCAG GACCAATGGG GAAGACCGGG     2450
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AAGCCAGGAC TTAATGGACA AAAAGGCCAG AAGGGAGAAA AAGGGAGTGG AAGCATGCAA   2510

AGACAATCTA ATACAGTCCG ACTGGTGGGT GGCAGCGGCC CTCACGAAGG CAGAGTGGAG   2570

ATTTTTCACG AAGGCCAGTG GGGTACGGTG TGTGACGACC GCTGGGAACT GCGTGGAGGA   2630

CTGGTCGTCT GCAGGAGCTT GGGATACAAA GGTGTTCAAA GTGTGCATAA GCGAGCTTAT   2690

TTTGGAAAAG GTACGGGTCC AATATGGCTG AATGAAGTAT TTTGTTTCGG GAAAGAGTCA   2750

TCCATTGAAG AGTGCAGAAT TAGACAGTGG GGTGTGAGAG CCTGTTCGCA CGACGAAGAT   2810

GCTGGGGGTC ACTTTGCACC TACATAATGC ATCATATTTT CATTCACATT TTTTAAACTG   2870

TTATAAAGTG ATTTTTTTCC TTTGCTTCAC TAAAATCAGC TTAATTAATA TTTAAGAAAC   2930

TAAGAATTTT ATCCACAGAA AAGGAATATT TAAAAATCAC TGGATAAACA TATAAAATAG   2990

CTTCATATTT GCTTCAAATA CCAGAACCAT TTCAACTTCT CTAGGTTTTT AAGTGGCTCG   3050

TGCCGAATTG ATCCCCTCAG GATATAGTAG TTTCGCTTTT GCATAGGGAG GGGGAAATGT   3110

AGTCTTATGC AATACTCTTG TAGTCTTGCA ACATGGTAAC GATGAGTTAG CAACATGCCT   3170

TACAAGGAGA GAAAAAGCAC CGTGCATGCC GATTGGTGGA AGTAAGGTGG TACGATCGTG   3230

CCTTATTAGG AAGGCAACAG ACGGGTCTGA CATGGATTGG ACGAACCACT GAATTCCGCA   3290

TTGCAGAGAT ATTGTATTTA AGTGCCTAGC TCGATACAGC AAACGCCATT TGACCATTCA   3350

CCACATTGGT GTGCACCTCC AAGCTTCACG CTGCCGCAAG CACTCAGGGC GCAAGGGCTG   3410

CTAAAGGAAG CGGAACACGT AGAAAGCCAG TCCGCAGAAA CGGTGCTGAC CCCGGATGAA   3470

TGTCAGCTAC TGGGCTATCT GGACAAGGGA AAACGCAAGC GCAAAGAGAA AGCAGGTAGC   3530

TTGCAGTGGG CTTACATGGC GATAGCTAGA CTGGGCGGTT TTATGGACAG CAAGCGAACC   3590

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GGAATTGCCA GCTGGGGCGC CCTCTGGTAA GGTTGGGAAG CCCTGCAAAG TAAACTGGAT    3650

GGCTTTCTTG CCGCCAAGGA TCTGATGGCG CAGGGGATCA AGATCTGATC AAGAGACAGG    3710

ATGAGGATCG TTTCGCATGA TTGAACAAGA TGGATTGCAC GCAGGTTCTC CGGCCGCTTG    3770

GGTGGAGAGG CTATTCGGCT ATGACTGGGC ACAACAGACA ATCGGCTGCT CTGATGCCGC    3830

CGTGTTCCGG CTGTCAGCGC AGGGGCGCCC GGTTCTTTTT GTCAAGACCG ACCTGTCCGG    3890

TGCCCTGAAT GAACTGCAGG ACGAGGCAGC GCGGCTATCG TGGCTGGCCA CGACGGGCGT    3950

TCCTTGCGCA GCTGTGCTCG ACGTTGTCAC TGAAGCGGGA AGGGACTGGC TGCTATTGGG    4010

CGAAGTGCCG GGGCAGGATC TCCTGTCATC TCACCTTGCT CCTGCCGAGA AAGTATCCAT    4070

CATGGCTGAT GCAATGCGGC GGCTGCATAC GCTTGATCCG GCTACCTGCC CATTCGACCA    4130

CCAAGCGAAA CATCGCATCG AGCGAGCACG TACTCGGATG GAAGCCGGTC TTGTCGATCA    4190

GGATGATCTG GACGAAGAGC ATCAGGGGCT CGCGCCAGCC GAACTGTTCG CCAGGCTCAA    4250

GGCGCGCATG CCCGACGGCG AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA    4310

TATCATGGTG GAAAATGGCC GCTTTTCTGG ATTCATCGAC TGTGGCCGGC TGGGTGTGGC    4370

GGACCGCTAT CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGGCGA    4430

ATGGGCTGAC CGCTTCCTCG TGCTTTACGG TATCGCCGCT CCCGATTCGC AGCGCATCGC    4490

CTTCTATCGC CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TAAAATAAAA    4550

GATTTTATTT AGTCTCCAGA AAAAGGGGGG AATGAAAGAC CCCACCTGTA GGTTTGGCAA    4610

GCTAGCTTAA GTAACGCCAT TTTGCAAGGC ATGGAAAAAT ACATAACTGA GAATAGAGAA    4670

GTTCAGATCA AGGTCAGGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA GGATATCTGT    4730
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GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT GGAACAGCTG AATATGGGCC   4790

AAACAGGATA TCTGTGGTAA GCAGTTCCTG CCCCGGCTCA GGGCCAAGAA CAGATGGTCC   4850

CCAGATGCGG TCCAGCCCTC AGCAGTTTCT AGAGAACCAT CAGATGTTTC CAGGGTGCCC   4910

CAAGGACCTG AAATGACCCT GTGCCTTATT TGAACTAACC AATCAGTTCG CTTCTCGCTT   4970

CTGTTCGCGC GCTTCTGCTC CCCGAGCTCA ATAAAAGAGC CCACAACCCC TCACTCGGGG   5030

CGCCAGTCCT CCGATTGACT GAGTCGCCCG GGTACCCGTG TATCCAATAA ACCCTCTTGC   5090

AGTTGCATCC GACTTGTGGT CTCGCTGTTC CTTGGGAGGG TCTCCTCTGA GTGATTGACT   5150

ACCCGTCAGC GGGGGTCTTT CATTTGG   5177

(2) INFORMATION FOR SEQ ID NO: 2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 400 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gln Trp Asp Asp Phe Pro Asp Gln Gln Glu Asp Thr Asp Ser
1   5   10   15

Cys Thr Glu Ser Val Lys Phe Asp Ala Arg Ser Val Thr Ala Leu Leu
                20   25   30

Pro Pro His Pro Lys Asn Gly Pro Thr Leu Gln Glu Arg Met Lys Ser
            35   40   45

Tyr Lys Thr Ala Leu Ile Thr Leu Tyr Leu Ile Val Phe Val Val Leu
        50   55   60

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Val Pro Ile Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
65                  70              75                  80


Lys Asn Cys Thr Val Gly Ser Val Asn Ala Asp Ile Ser Pro Ser Pro
                85              90                  95


Glu Gly Lys Gly Asn Gly Ser Glu Asp Glu Met Arg Phe Arg Glu Ala
                100             105             110


Val Met Glu Arg Met Ser Asn Met Glu Ser Arg Ile Gln Tyr Leu Ser
            115             120             125


Asp Asn Glu Ala Asn Leu Leu Asp Ala Lys Asn Phe Gln Asn Phe Ser
    130             135             140


Ile Thr Thr Asp Gln Arg Phe Asn Asp Val Leu Phe Gln Leu Asn Ser
145             150             155             160


Leu Leu Ser Ser Ile Gln Glu His Glu Asn Ile Ile Gly Asp Ile Ser
                165             170             175


Lys Ser Leu Val Gly Leu Asn Thr Thr Val Leu Asp Leu Gln Phe Ser
                180             185             190


Ile Glu Thr Leu Asn Gly Arg Val Gln Glu Asn Ala Phe Lys Gln Gln
            195             200             205


Glu Glu Met Arg Lys Leu Glu Glu Arg Ile Tyr Asn Ala Ser Ala Glu
    210             215             220


Ile Lys Ser Leu Asp Glu Lys Gln Val Tyr Leu Glu Gln Glu Ile Lys
225             230             235             240


Gly Glu Met Lys Leu Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu Lys
                245             250             255


Asp Trp Glu His Ser Gln Thr Leu Lys Asn Ile Thr Leu Leu Gln Gly
                260             265             270
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Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser
       275   280   285

Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr
       290   295   300

Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro
305   310   315   320

Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe
           325   330   335

Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr
       340   345   350

Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met
       355   360   365

Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala
       370   375   380

Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu
385   390   395   400